

A. DEC100X

1644

P#6

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,088

DATE: 05/09/2000
TIME: 06:36:01

Input Set: I382088.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

PS

1 <110> APPLICANT: Hope, Ernest G
2 Negrin, Robert
3 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTECTING ORGANS, TISSUE
4 AND CELLS FROM IMMUNE SYSTEM-MEDIATED DAMAGE
5 <130> FILE REFERENCE: A-67031-1/RFT
6 <140> CURRENT APPLICATION NUMBER: US/09/382,088
7 <141> CURRENT FILING DATE: 1999-08-24
8 <150> EARLIER APPLICATION NUMBER: 60/097,640
9 <151> EARLIER FILING DATE: 1998-08-24
10 <160> NUMBER OF SEQ ID NOS: 30
11 <170> SOFTWARE: PatentIn Ver. 2.1
12 <210> SEQ ID NO 1
13 <211> LENGTH: 9
14 <212> TYPE: PRT
15 <213> ORGANISM: Artificial Sequence
16 <220> FEATURE:
17 <221> NAME/KEY: SITE
18 <222> LOCATION: (1)
19 <223> OTHER INFORMATION: X at position 1 can be V, L, A or T.
20 <220> FEATURE:
21 <221> NAME/KEY: SITE
22 <222> LOCATION: (2)
23 <223> OTHER INFORMATION: X at position 2 can be L or H.
24 <220> FEATURE:
25 <221> NAME/KEY: SITE
26 <222> LOCATION: (3)
27 <223> OTHER INFORMATION: X at position 3 can be S or V.
28 <220> FEATURE:
29 <221> NAME/KEY: SITE
30 <222> LOCATION: (4)
31 <223> OTHER INFORMATION: X at position 4 can be D or E.
32 <220> FEATURE:
33 <221> NAME/KEY: SITE
34 <222> LOCATION: (5)
35 <223> OTHER INFORMATION: X at position 5 can be Q, K or R.
36 <220> FEATURE:
37 <221> NAME/KEY: SITE
38 <222> LOCATION: (6)
39 <223> OTHER INFORMATION: X at position 6 can be L or V.
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
42 sequence.
43 <400> SEQUENCE: 1
44 Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg

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W--OK

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45 1 5

46 <210> SEQ ID NO 2

47 <211> LENGTH: 9

48 <212> TYPE: PRT

49 <213> ORGANISM: Artificial Sequence

50 <220> FEATURE:

51 <221> NAME/KEY: SITE

52 <222> LOCATION: (1)..(3)

53 <223> OTHER INFORMATION: X at positions 1, 2, or 3 can be any amino acid.

54 <220> FEATURE:

55 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus

56 sequence.

57 <400> SEQUENCE: 2

58 Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg

59 1 5

60 <210> SEQ ID NO 3

61 <211> LENGTH: 9

62 <212> TYPE: PRT

63 <213> ORGANISM: Homo sapiens

64 <400> SEQUENCE: 3

65 Ala Val Leu Ser Ala Glu Gln Leu Arg

66 1 5

67 <210> SEQ ID NO 4

68 <211> LENGTH: 1254

69 <212> TYPE: DNA

70 <213> ORGANISM: Homo sapiens

71 <400> SEQUENCE: 4

72 cggtccact tctttggaca tctccggcgt cggggaccat gacgcctctt cgactcaagg 60

73 ttccgctggt gtgaccgtct cgggtcgtgt ccggaccgga agtcggacat agtccgttac 120

74 cggttcctgt gtccgtcacc tcttgtagga ccacagtggg caccaccacc ggagcagcga 180

75 cccagagcac agcgaccgcg cggtccgctg gtgccgcagc gtccggttcc gtcacgactc 240

76 gcggctcctc acgcgagaga ggaagaccgc tggaaatagg aggaccgaca ccgggaccgt 300

77 gacgcgtgct tcctccacgt gcggccggac ccactcgacg acgcgagtga gtcgttgagc 360

78 tgccgcgctg tgcactggac ctccgaccgc tcggctgaca tgctgggtc gagtactcgt 420

79 aagcgactac tgaagcacgc gtcgtcgttc gtcgtgatgt tgacgtcgt gaggttctag 480

80 ttgaagggcc tgcgcgctcg cgcgacgtca ggtagtgtgt caccgcgcgc gtcgcgcgcg ggacgatcag 540

81 ctgccgttcg acgggctcca gtggttcctg cacctcgcgt gtcgcgcgcg ggacgatcag 600

82 ttgcggtaca agaagttcgg tgtgacccta ctctttaagg tgggtgttcta ccacctgttg 660

83 gcaccgaagt accactgagc caggatatga caccacaat gctactacgt ggctgttccg 720

84 gagatgttga tgatgctgct gctcttcctc ttcgacgtcg accacctcta cggggaccga 780

85 gtgttcgaga ggtcggagta gtaggagtag ggggtagtgc acctcgagga gtcgcggaa 840

86 cttttcgacg attggtttct cgctcgacttc tagacctacc ctttctacgt cttcttccga 900

87 caacggtaga ggaacgggtt cccacaccac ctccactggg tactggacgt ctttgtggac 960

88 cgaccgcgacc cggactgact ccggttaactg ttcttggtcc ggctgaatag tgcgtacaga 1020

89 ccgttcttcc tagacatgga ccggtcacac aaggtgcggg ggcggaaact caacctgtgt 1080

90 ctaccgttgg ggaaactggt cctgtagatg cccgcgctcc tcgacgcgtc ggggttcgac 1140

91 aagatgcggc tgggtgggaa gtagaaggac cagccctgt gggtttcgcc gagggacgat 1200

92 aagtaaccgc cggaccaggc cgagttccca ctgttctacg ctctgctcaa tate 1254

93 <210> SEQ ID NO 5

94 <211> LENGTH: 1254

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RAW SEQUENCE LISTING
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95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
97 <220> FEATURE:
98 <221> NAME/KEY: CDS
99 <222> LOCATION: (1)..(1251)
100 <400> SEQUENCE: 5
101   atg cgc tct ctc ctt ctg ggc acc tta tgc ctc ctg gct gtg gcc ctg   48
102   Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
103       1               5               10               15
104   gca gcc gag gtg aag aaa cct gta gag gcc gca gcc cct ggt act gcg   96
105   Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
106       20               25               30
107   gag aag ctg agt tcc aag gcg acc aca ctg gca gag ccc agc aca ggc
108   Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
109       35               40               45
110   ctg gcc ttc agc ctg tat cag gca atg gcc aag gac cag gca gtg
111   Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
112       50               55               60
113   aac atc ctg gtg tca ccc gtg gtg gtg gcc tcg tcg ctg ggt ctc gtg
114   Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
115       65               70               75               80
116   tcg ctg ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg   288
117   Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
118       85               90               95
119   agc gcc gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggt gag   336
120   Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
121       100              105              110
122   ctg ctg cgc tca ctc agc aac tcg acg gcg cgc aac gtg acc tgg aag   384
123   Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
124       115              120              125
125   ctg ggc agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac   432
126   Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
127       130              135              140
128   ttc gtg gcg agc agc aag cag cac tac aac tgc gag cac tcc aag atc   480
129   Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
130       145              150              155              160
131   aac ttc ccg gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc   528
132   Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
133       165              170              175
134   gcg cag acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag   576
135   Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
136       180              185              190
137   agc acg gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac   624
138   Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
139       195              200              205
140   tgg gat gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg   672
141   Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
142       210              215              220
143   gtg act cgg tcc tat act gtg ggt gtt acg atg atg cac cgg aca ggc   720
144   Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly

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145      225      230      235      240
146      ctc tac aac tac tac gac gac gag aag gag aag ctg cag ctg gtg gag 768
147      Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
148      245      250      255
149      atg ccc ctg gct cac aag ctc tcc agc ctc atc atc ctc atg ccc cat 816
150      Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
151      260      265      270
152      cac gtg gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag 864
153      His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
154      275      280      285
155      ctg aag atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc 912
156      Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
157      290      295      300
158      ttg ccc aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg 960
159      Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
160      305      310      315      320
161      gct ggg ctg ggc ctg act gag gcc att gac aag aac aag gcc gac tta 1008
162      Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
163      325      330      335
164      tca cgc atg tct ggc aag aag gat ctg tac ctg gcc agt gtg ttc cac 1056
165      Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
166      340      345      350
167      gcc acc gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac 1104
168      Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
169      355      360      365
170      atc tac ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac 1152
171      Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
172      370      375      380
173      cac ccc ttc atc ttc ctg gtg cgg gac acc caa agc ggc tcc ctg cta 1200
174      His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
175      385      390      395      400
176      ttc att ggg cgc ctg gtc cgg ctc aag ggt gac aag atg cga gac gag 1248
177      Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
178      405      410      415
179      tta tag
180      Leu 1254
181      <210> SEQ ID NO 6
182      <211> LENGTH: 417
183      <212> TYPE: PRT
184      <213> ORGANISM: Homo sapiens
185      <400> SEQUENCE: 6
186      Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
187      1 5 10 15
188      Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
189      20 25 30
190      Glu Lys Leu Ser Ser Lys Ala Thr Leu Ala Glu Pro Ser Thr Gly
191      35 40 45
192      Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
193      50 55 60
194      Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val

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195      65      70      75      80
196      Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
197      85      90      95
198      Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
199      100      105      110
200      Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
201      115      120      125
202      Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
203      130      135      140
204      Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
205      145      150      155      160
206      Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
207      165      170      175
208      Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
209      180      185      190
210      Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
211      195      200      205
212      Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
213      210      215      220
214      Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
215      225      230      235      240
216      Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
217      245      250      255
218      Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
219      260      265      270
220      His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
221      275      280      285
222      Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
223      290      295      300
224      Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
225      305      310      315      320
226      Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
227      325      330      335
228      Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
229      340      345      350
230      Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
231      355      360      365
232      Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
233      370      375      380
234      His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
235      385      390      395      400
236      Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
237      405      410      415
238      Leu

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239 <210> SEQ ID NO 7

240 <211> LENGTH: 9

241 <212> TYPE: PRT

242 <213> ORGANISM: Artificial Sequence

243 <220> FEATURE:

244 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/382,088DATE: 05/09/2000
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Line ? Error/Warning

Original Text

44 W "N" or "Xaa" used: Feature required
58 W "N" or "Xaa" used: Feature required
299 W "N" or "Xaa" used: Feature required
321 W "N" or "Xaa" used: Feature required

Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg
Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg
Ala Val Leu Ser Ala Xaa Xaa Leu Arg
Ala Xaa Leu Ser Ala Glu Xaa Xaa Arg